Amendments to the Claims

1-77. (Cancelled)

78. (Previously Presented) A method of introgressing an allele into a soybean plant comprising

(A) crossing at least one SCN resistant soybean plant having an rhgl SCN resistant allele with at least one SCN sensitive soybean plant having an rhgl SCN sensitive allele in order to form a segregating population,

(B) screening said segregating population with one or more nucleic acid markers to determine if one or more soybean plants from said segregating population contains a deletion of 19 nucleotides corresponding to SEQ ID NO: 2 and encompassing position 48881, and

(C) selecting, if present, one or more soybean plants of said segregating population containing said deletion.

79. (Currently Amended) The method according to claim 78, wherein said one or more soybean plants ~~members~~ of said segregating population have a yellow soybean seed.

80.-85. (Cancelled)

86. (Previously Presented) A method of introgressing an allele from a first soybean plant comprising a polymorphism relative to a second soybean plant into a selected soybean plant comprising screening with one or more nucleic acid markers a population of soybean plants formed by a cross of said first and said second soybean plant and selecting a soybean plant, wherein said allele is an allele having one or more polymorphisms in a protein coding region corresponding to nucleotides 45163 to 45314, 45450 to 45509, 46941 to 48763 or 48975 to 49573 of SEQ ID NO: 2, thereby introgressing said allele from said first soybean plant comprising a polymorphism into said selected soybean plant.

87. (Previously Presented) The method according to claim 86, wherein said polymorphisms are selected from the group consisting of 45173, 45309, 47057, 47140, 47208, 47571, 47617, 47796, 47856, 47937, 48012, 48060, 48073, 48135, 48279, 48413, 48681, 49012, and 49316 of SEQ ID NO: 2.

88. (Previously Presented) The method according to claim 86, wherein said introgressing said allele into said selected soybean plant results in a yellow soybean seed.

89. (Previously Presented) A method of introgressing an allele comprising a polymorphism into a soybean plant lacking said polymorphism comprising screening a population of soybean plants with one or more nucleic acid markers and selecting a soybean plant, wherein said one or more nucleic acid markers are capable of detecting one or more polymorphisms located at a position in SEQ ID NO: 2 selected from the group consisting of 45173, 45309, 47057, 47140, 47208, 47571, 47617, 47796, 47856, 47937, 48012, 48060, 48073, 48135, 48279, 48413, 48681, 49012, and 49316,

thereby selecting a soybean plant comprising said polymorphism.

90. (Previously Presented) The method according to claim 89, wherein said introgressing said allele comprising a polymorphism into said soybean plant results in one or more soybean plant having a yellow soybean seed and said polymorphism.

91. (Currently Amended) A method of introgressing an rhg1 SCN resistant allele into a non-resistant soybean plant comprising

(A) crossing at least one SCN resistant soybean plant having [[an]] said rhg1 SCN resistant allele corresponding to an rhg1 SCN resistant allele present in Peking with at least one SCN sensitive soybean plant having an rhgl SCN sensitive allele in order to form a segregating population,

(B) screening said segregating population with one or more nucleic acid markers to identify said rhg1 SCN resistant allele, wherein said one or more nucleic acid markers are capable of detecting a polymorphism located at a position in SEQ ID NO: 2 corresponding to nucleotides between 45163 and 49573, and

(C) selecting one or more members of said segregating population having said rhgl SCN resistant allele.

92. (Previously Presented) The method according to claim 91, wherein said one or more members of said segregating population have a yellow soybean seed.

93. (Previously Presented) The method according to claim 91, wherein said one or more nucleic acid markers are capable of detecting a single nucleotide polymorphism or INDEL mutation.

94. (Previously Presented) The method according to claim 91, wherein said one or more nucleic acid markers are capable of detecting one or more polymorphisms located at a position in SEQ ID NO: 2 selected from the group consisting of 45173, 45309, 47057, 47140, 47208, 47571, 47617, 47796, 47856, 47937, 48012, 48060, 48073, 48135, 48279, 48413, 48681, 49012, 49316, and 46703.

95. (Previously Presented) The method according to claim 91, wherein said one or more nucleic acid markers are capable of detecting single nucleotide polymorphisms.

96. (Previously Presented) The method according to claim 95, wherein said single nucleotide polymorphisms are located at a position in SEQ ID NO: 2 selected from the group consisting of 45173, 45309, 47057, 47140, 47208, 47571, 47617, 47796, 47856, 47937, 48012, 48060, 48073, 48135, 48279, 48413, 48681, 49012, and 49316.

97. (Previously Presented) The method according to claim 91, wherein said one or more nucleic acid markers are capable of detecting INDEL mutations.

98.-106. (Cancelled)